

Job Title: # of hours:

Prof. Dr. J. J. G. S. S.

BLASTN 2.2.16+

References

Stephen F. Alcantara, Thomas L. Woodin, Alejandro A. Joraffac, Jiahezi Jiang, Sheng Wang, John Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:323-335.

SID: 20C41761019

Database: All GenBank/EMBL/CCDS/RefSeq sequences (not rc, X1, G1,
GCS, environmental samples or phase 0, 1 or 2 HUS sequences)
7,318,665 sequences; 24,754,383,457 total letters

If you have any questions or concerns with the results of this course

PLEASE REFER TO THE CLASS PAGE

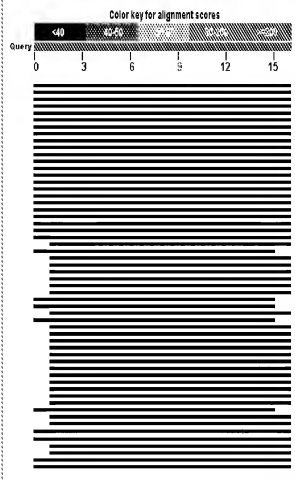
1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 26

245V=

 $\lambda_{\text{avg}} = 1.6$

Distribution of 158 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



2005-05-15 14:25:25

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¹Aggravated assault is a violent crime.

(Click on boxes in next column)

[illegible]

| | | | | |
|------|------|-----|----|-------|
| 30.2 | 30.7 | 90% | 30 | >100% |
| 30.2 | 30.5 | 99% | 33 | >100% |
| 30.2 | 30.2 | 99% | 35 | >100% |
| 30.1 | 30.7 | 90% | 34 | >100% |
| 30.3 | 30.2 | 97% | 38 | >100% |
| 30.2 | 30.2 | 99% | 33 | >100% |
| 30.2 | 30.2 | 99% | 35 | >100% |
| 30.2 | 30.2 | 99% | 35 | >100% |
| 30.2 | 30.5 | 98% | 34 | >100% |
| 30.2 | 30.2 | 97% | 38 | >100% |

Get selected sequences Select all Deselect all Distance tree of results

| | | |
|--------------|------------------|--------|
| Ques v 1 | 0000000000000000 | 16 |
| 16jet 101900 | 0000000000000000 | 161900 |

| | | |
|---------------|------------------|------|
| Query 1 | GTGTCAGAGCGGACCA | 16 |
| | | |
| Subject 17292 | GTATCAAGTCAACG | 1407 |

| | | |
|-------------|-------------------|----|
| Query 1 | GTGCTGAGGCTGAGCTA | 16 |
| | | |
| Strain 209b | GTGCTGAGGCTGAGCTA | 16 |

| | | |
|-------------|-----------------|----|
| Query 1 | GGTTCAGGCTCAACA | 16 |
| | : : : : : : | |
| Sliver 1055 | GGTTCAGGCTCAACA | 16 |

| | | |
|-------------|-------------------|------|
| (racc: 1 | GTCTTAAAGCTTAAACA | 14 |
| | | |
| (bncr: 1430 | ATGACAAAGCTTAAACA | 1515 |

```

(over 1  GTCFACCTCAGCA  36
          TTTTCTTTTCTT
(bact 1973  GTGCTGAGCTGCTG  152

```

DATE: 07/07/2008 10:00:00

Score = 15.3 bits (17), Expect = 612
Identical seq = 13/13 (100%), gaps = 3/13 (23%)
Strand = Plus/Minus

Query 2 GGTTCAGACCTCAAC 14
|||||
Subject 10989791 GGTTCAGACCTCAAC 10989791

■ [U04612 \(U04612.1\)](#) Same DNA sequence from clone W1-116923 on chromosome 1, complete sequence
Length = 10727

Score = 15.1 bits (15), Expect = 9.3
Identical seq = 10/10 (100%), gaps = 0/10 (0%)
Strand = Plus/Minus

Query 2 GGTTCAGACCTCAAC 14
|||||
Subject 10713 GGTTCAGACCTCAAC 10713

■ [U04613 \(U04613.1\)](#) Truncated cDNA sequence for DNA polymerase alpha catalytic subunit, partial cds
Length = 6912

Score = 15.1 bits (15), Expect = 9.3
Identical seq = 10/10 (100%), gaps = 0/10 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 14
|||||
Subject 170 GGTTCAGACCTCAAC 170

■ [U04614 \(U04614.1\)](#) Same sequence chromosome 9 clone C10-20223, complete sequence
Length = 4455

Score = 15.1 bits (15), Expect = 9.3
Identical seq = 10/10 (100%), gaps = 0/10 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 14
|||||
Subject 17449 GGTTCAGACCTCAAC 17449

■ [U04615 \(U04615.1\)](#) Acetabularia thaliana DNA chromosome 4, coding fragment no. 43
Length = 10375

Score = 15.1 bits (15), Expect = 9.3
Identical seq = 10/10 (100%), gaps = 0/10 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 14
|||||
Subject 12616 GGTTCAGACCTCAAC 12617

■ [U04616 \(U04616.1\)](#) Arabidopsis thaliana DNA chromosome 1, NC clone F2631, cDNA1
Length = 11607

Score = 15.2 bits (16), Expect = 9.1
Identical seq = 16/15 (100%), gaps = 0/15 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 16
|||||
Subject 91704 GGTTCAGACCTCAAC 91811

■ [U04617 \(U04617.1\)](#) Same sequence chromosome 11, clone F261-Z1707C, complete sequence
Length = 15101

Score = 15.2 bits (16), Expect = 9.1
Identical seq = 16/15 (100%), gaps = 0/15 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 16
|||||
Subject 16913 GGTTCAGACCTCAAC 16915

■ [U04618 \(U04618.1\)](#) Arabidopsis thaliana sp. BPC #402 DNA, complete genome
Length = 317413

For Alignments for this subject sequence see:
6 values from [FASTA](#) [FASTA](#) [FASTA](#)
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)

Features in this part of subject sequence:
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)

Score = 15.2 bits (16), Expect = 9.3
Identical seq = 16/15 (100%), gaps = 0/15 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 16
|||||
Subject 746713 GGTTCAGACCTCAAC 746628

Features in this part of subject sequence:
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)

Score = 15.2 bits (16), Expect = 103
Identical seq = 16/15 (100%), gaps = 0/15 (0%)
Strand = Plus/Minus

Query 1 GGTTCAGACCTCAAC 16
|||||
Subject 107149 GGTTCAGACCTCAAC 1071103

Features in this part of subject sequence:
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)
[FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#) [FASTA](#)

Score = 15.3 bits (17), Expect = 612
Identical seq = 13/13 (100%), gaps = 3/13 (23%)
Strand = Plus/Minus

2016 2117 GREGORY ET AL. 2117

[illegible]

Gene ID: 557578, CDS: 557578, 1, 218485, DNA product from transcript G14566-02

Score = 34.2 bits (11), Expect = 35
Identical = 14/15 (93%), Gaps = 0/15 (0%)
Standard+Plus/Plus

| | | | |
|----------|------|-----------------|------|
| Genotype | Z | TGTCGAGGCGGACCA | 16 |
| | | | |
| Strict | 1000 | TGTCGAGGCGGACCA | 1000 |

[illegible][illegible]

Features in this part of subject covered:
 CONSTRUCTION OF A. 2.000.000

Score = 74.2 bits (51), Expect = 35
Identical = 15/15 (100%), Gaps = 0/15 (0%)
Standardizing Values

| | | | |
|--------|--------|---------------|--------|
| Query | 1 | CGTTCGAGCCGAC | 15 |
| | | | |
| Refseq | 786531 | GATTGAGCCGAC | 786535 |

Previous in this part of subject sequence:
 non-organic nitrogenous material

Score = 15.3 bits (15%, Expect = 612)
Identities = 12/13 (100%), Gaps = 0/13 (0%)
Max. Ambig. Nucleotides = 0

| | | |
|----------------|--------------|--------|
| Query 2 | INTCAGCTGGA | 16 |
| | | |
| Subject 004189 | TGTGGACCTGAA | 694774 |

[illegible]

DATE: 10/12/11 TIME: 11:10:11 AM BY: 101011-111011 (Name correct)
1/2 of page 10/12/11

Score = 30.2 bits (13), Expect = 35
 Identical = 15/15 (100%), Gaps = 0/15 (0%)
 Strand: Plus/Minus

| | | | |
|-------|------|-------------------|------|
| Genes | 2 | 7GTCAGAGGCAATACCA | 25 |
| | | | |
| Genes | 7476 | TTTCTGACCTGACCA | 7476 |

▶ [bioRxiv preprint doi: <https://doi.org/10.1101/2019.03.11.288413>; this version posted March 11, 2019. The copyright holder for this preprint \(which was not certified by peer review\) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.](#)

WWW.US-CIVILIAN-CHALLENGE.S : rich21-0706.9 (Basic verio)
(10 or lower Public Link)

Genus = 30.2 bits (15), Export = 39
 Identifiers = 15/15 (100%), Genes = 0/15 (0%)
 Species = 0/15 (0%)

| | | |
|------------|----------------|------|
| Query 7 | YGTGAGGCTAATCA | T6 |
| | | |
| Stick_2659 | TGTGAAGTTCACCG | C-48 |

▣ [Gill193101.1](#) Helicobacter pylori Ss470, complete genome
taxid:1609518

See assignments for this subject sequence by:
 1. value 2000 2000 2000
 2. value 2000 2000 2000

Previous in this part of subject sequence:
 1. Introduction to the subject

```
Scots = 30.1 bits (15, Export = 33
Identical = 15/15 (100%), Gaps = 0/15 (0%)
Xxx-xx-xxxx-xxxx
```

| | | |
|--------------|----------------|--------|
| Query 2 | INITIALS | 16 |
| | | |
| Sider 447036 | VGNC3845734876 | 447036 |

Features in this part of adjacent regions are symmetrical, positive.

Score = 26.3 Data (33), Expect = 412
Identification = 13.1 (100%), Gaps = 9/13 (69)
StandardPlusPlus

[illegible][illegible]

Features in this part of subject sequence:
coll. 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2

Spice = 30.2 bits (15%, Exponent = 39)
 16-bit integer = 15/15 (100%), Gaps = 0/15 (0%)
 8-bit integer = 15/15 (100%)

Query 7: ESTIMATING THE NUMBER OF

<http://at.mh-heidelberg.de/doi/10.1007/978-3-642-00000-0>

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 1 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Streptococcus carnosus strain DSM 12991, complete genome
Length: 1553390

Matches in this part of subject sequence:
TCTGAGTTCAGAC 154201

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Genie testis c10c11-57616.9 (c10c11-47415.9), mRNA

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 1 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Ovis montanus, chromosome X, complete sequence
Length: 14146

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Interleukin-28A sequence from clone 6661-3033 in liverpool group
in complete sequence
Length: 15708

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Rat trophoblast 88C clone (R251-6489) from chromosome X, complete
sequence
Length: 174491

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Arabidopsis thaliana, complete genome
Length: 1899910

Matches in this part of subject sequence:
TCTGAGTTCAGAC 154201

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Ovis montanus c10c11-57616.9, whole genome shotgun sequence
Length: 16466

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'


Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

NCBI Benchmarks (2018) **NCBI** Arabidopsis thaliana, complete genome
Length: 1899910

Matches in this part of subject sequence:
TCTGAGTTCAGAC 154201

Score = 30.2 bits (15), Expect = 39
Identical = 25/25 (100%), gaps = 0/25 (0%)
Strand: 5' to 3'

Query: 2 TCTGAGTTCAGAC 16
11111111111111111111
Subject: 154201 TCTGAGTTCAGAC 154204

■ [Download](#)  Download this sequence (6,040 bp, complete genome)
Length=6040bp

Sort alignments for this subject sequence by:
 1. Value: Score (default) | 2. Size
 Descending | Ascending | Default (Score, Descending)

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.3 bits (11), Expect = 35
 Identical = 15/15 (100%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 1 [TTTAAAGCTGACAC](#) 16
 +[+][+][+][+]
 Subject 339491 [TTTAAAGCTGACAC](#) 339491

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.3 bits (11), Expect = 352
 Identical = 15/15 (100%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 2 [TTTAAAGCTGAC](#) 15
 +[+][+][+][+]
 Subject 339491 [TTTAAAGCTGACAC](#) 339491

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.3 bits (11), Expect = 432
 Identical = 14/15 (93%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 3 [TTTAAAGCTGACAC](#) 16
 +[+][+][+][+]
 Subject 340441 [TTTAAAGCTGACAC](#) 340441

■ [Download](#)  Download this sequence from clone F211-1938 in linkage map
 1. Complete sequence
 Length=1973bp

Sort alignments for this subject sequence by:
 1. Value: Score (default) | 2. Size
 Descending | Ascending | Default (Score, Descending)

Score = 76.1 bits (11), Expect = 39
 Identical = 14/15 (93%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 2 [TTTAAAGCTGACAC](#) 16
 +[+][+][+][+]
 Subject 1074 [TTTAAAGCTGACAC](#) 51239

Score = 76.1 bits (11), Expect = 255
 Identical = 14/15 (93%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 3 [TTTAAAGCTGACAC](#) 16
 +[+][+][+][+]
 Subject 1710 [TTTAAAGCTGACAC](#) 1741

■ [Download](#)  Download this sequence from clone F211-1938 in linkage map
 Length=1042bp

Sort alignments for this subject sequence by:
 1. Value: Score (default) | 2. Size
 Descending | Ascending | Default (Score, Descending)

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.2 bits (11), Expect = 39
 Identical = 15/15 (100%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 1 [TTTAAAGCTGACAC](#) 16
 +[+][+][+][+]
 Subject 106550 [TTTAAAGCTGACAC](#) 106415

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.3 bits (11), Expect = 155
 Identical = 14/15 (93%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 1 [TTTAAAGCTGAC](#) 15
 +[+][+][+][+]
 Subject 341709 [TTTAAAGCTGAC](#) 341705

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.1 bits (11), Expect = 255
 Identical = 14/15 (93%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 1 [TTTAAAGCTGAC](#) 15
 +[+][+][+][+]
 Subject 678460 [TTTAAAGCTGAC](#) 678449

Features in this part of subject sequence:
[View: GenomicMap](#)

Score = 76.2 bits (11), Expect = 155
 Identical = 14/15 (93%), gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 3 [TTTAAAGCTGACAC](#) 16
 +[+][+][+][+]
 Subject 1342095 [TTTAAAGCTGACAC](#) 1342104

Features in this part of subject sequence:
0602031203

Score = 24.2 bits (14), Expect = .05
Identical = 14/14 (100%), gaps = 0/12 (0%)
Strand=9/m7plus

Query 3 CTGACCTGACCA 16
111111111111
Subject 02080415 CTGACCTGACCA 02080415

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 20.3 bits (12), Expect = 0.17
Identical = 12/12 (100%), gaps = 0/12 (0%)
Strand=9/m7plus

Query 1 ATGTCAGATGCA 12
111111111111
Subject 07007019 ATGTCAGATGCA 07007019

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 26.8 bits (13), Expect = 0.02
Identical = 12/12 (100%), gaps = 0/12 (0%)
Strand=9/m7plus

Query 6 TTAGGCTGACCA 16
111111111111
Subject 1801471 TTAGGCTGACCA 1801471

Features in this part of subject sequence:
0602031203...0602031203
0602031203...0602031203

Score = 16.3 bits (8), Expect = 0.12
Identical = 13/13 (100%), gaps = 0/13 (0%)
Strand=9/m7plus

Query 6 TTAGGCTGACCA 16
111111111111
Subject 14707065 TTAGGCTGACCA 14707065

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 24.3 bits (13), Expect = 0.02
Identical = 13/13 (100%), gaps = 0/13 (0%)
Strand=9/m7plus

Query 9 TTAGGCTGACCA 16
111111111111
Subject 18441549 TTAGGCTGACCA 18441549

  GenBank accession number 02080415, complete sequence
1102030003...0602031203

Best alignment for this subject sequence is:
T 1419 T 0602031203...0602031203
Q 0602031203...0602031203

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 20.2 bits (11), Expect = .39
Identical = 15/15 (100%), gaps = 0/15 (0%)
Strand=9/m7plus

Query 7 CTGACCTGACCA 16
111111111111
Subject 02040720 CTGACCTGACCA 02040720

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 23.1 bits (14), Expect = .05
Identical = 14/14 (100%), gaps = 0/14 (0%)
Strand=9/m7plus

Query 1 CTGACCTGACCA 16
111111111111
Subject 02143740 CTGACCTGACCA 02143740

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 26.2 bits (14), Expect = .03
Identical = 14/14 (100%), gaps = 0/14 (0%)
Strand=9/m7plus

Query 1 CTGACCTGACCA 16
111111111111
Subject 11167782 CTGACCTGACCA 11167782

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 20.1 bits (14), Expect = .25
Identical = 14/14 (100%), gaps = 0/14 (0%)
Strand=9/m7plus

Query 2 CTGACCTGACCA 16
111111111111
Subject 11193317 CTGACCTGACCA 11193317

Features in this part of subject sequence:
1102030003...0602031203
1102030003...0602031203

Score = 26.8 bits (13), Expect = 0.01
Identical = 13/13 (100%), gaps = 0/13 (0%)
Strand=9/m7plus

Features in this part of subject sequence:

ORF1
 Score = 39.3 bits (15), Expect = 39
 Identical = 10/15 (66%), gaps = 0/15 (0%)
 Strand=+/-inFrame
 Query: 1 TTTTAAAGCTTAAACA 14
 11111111111111111111
 Subject: 557138 TTTTAAAGCTTAAACA 557154

Features in this part of subject sequence:
 Cytosine-rich intercalated repeat RNA repeat (Cytosine-rich)

Score = 26.3 bits (11), Expect = 417
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 4 TTTTAAAGCTTAAACA 14
 11111111111111111111
 Subject: 2517679 TTTTAAAGCTTAAACA 2517842

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

See all genes in this subject sequence by:
 a) view [Genes](#) [Proteins](#) [Annotations](#)
 b) view [Genes](#) [Proteins](#) [Annotations](#) [Statistics](#)

Features in this part of subject sequence:
 Cytosine-rich intercalated

Score = 26.3 bits (11), Expect = 39
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 1 TTTTAAAGCTTAAACA 14
 11111111111111111111
 Subject: 458418 TTTTAAAGCTTAAACA 458432

Features in this part of subject sequence:
 Cytosine-rich intercalated

Score = 25.3 bits (11), Expect = 51.1
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 4 TTTTAAAGCTTAAACA 14
 11111111111111111111
 Subject: 1480787 TTTTAAAGCTTAAACA 1480792

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

Score = 26.1 bits (11), Expect = 39
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 1 TTTTAAAGCTTAAACA 13
 11111111111111111111
 Subject: 604 TTTTAAAGCTTAAACA 609

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

Score = 30.3 bits (11), Expect = 39
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 2 TTTTAAAGCTTAAACA 16
 11111111111111111111
 Subject: 567 TTTTAAAGCTTAAACA 567

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

Score = 26.1 bits (11), Expect = 39
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 2 TTTTAAAGCTTAAACA 14
 11111111111111111111
 Subject: 616 TTTTAAAGCTTAAACA 621

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

Score = 30.1 bits (11), Expect = 39
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 1 TTTTAAAGCTTAAACA 15
 11111111111111111111
 Subject: 6666 TTTTAAAGCTTAAACA 6672

U011100.1 **NC_001000000** **U011100.1** **NC_001000000** **U011100.1** **NC_001000000**
 complete genome
 length=153865

Score = 26.3 bits (11), Expect = 39
 Identical = 10/11 (90%), gaps = 0/11 (0%)
 Strand=+/-inFrame

Query: 2 TTTTAAAGCTTAAACA 16
 11111111111111111111
 Subject: 375 TTTTAAAGCTTAAACA 380

20101 145543 YETC346T2447A 145529

At 09:13:06Z /usr/sbin/rsyncd can't connect to host 192.168.1.100: connection refused
rsyncd

Score = 70.2 bits (11), Expect = 35
Identical = 14/16 (88%), Gaps = 0/16 (0%)
Standard/Plus/Minus

| | | | |
|-------|-------|----------------|-------|
| Q2017 | 2 | TGTCAGAGTCAGCA | 36 |
| | | | |
| dbnet | STORE | TGTCAGAGTCAGCA | 61870 |

▣ [U04613026.101](#) [Mus musculus thymosin \$\alpha_2\$, clone MP28-31ZC2, complete sequence](#)
Length=724556

```
Score = 34.2 bits (13), Expect = 35
Overlapped = 15/15 (100%), Gaps = 0/15 (0%)
Diamond-Plus/Minus
```

| | | | |
|-------|--------|------------------|------|
| Query | 2 | YGTCTAGAGCCAAACA | 16 |
| | | | |
| fbact | 145583 | ATCTCAAGCCCAAGC | 1455 |

1. **chr12:23,110,111** Has nucleolar chromosome 12P11.2-12P12, complete sequence
length=21,702

Score alignment for this subject sequence by:
 % value score 200000 1000000
 Score: 1000000 1000000 1000000 1000000

Score = 30.2 bits (11), Expect = 35
Identical = 14/15 (93%), gaps = 0/15 (0%)
Standalone only

| | | | |
|----------|-------|-----------------|-------|
| Genotype | 7 | TGTTTACGCTTACCA | 36 |
| | | | |
| Probe | 57162 | TGTTTACGCTTACCA | 67756 |


```
Score = 25.3 bits (11), Expect = 412
Ident: 100% (1000), Gaps = 0/13 (0%)
Clc: codon-bias: 0.000
```

| | | | |
|---------|--------|---------------|--------|
| Query | 2 | YETCRAGSGTQAA | 24 |
| | | | |
| Subject | 255679 | TGTCAAGSGTCAA | 255657 |

```
> readAFAST("D:\B06-665C4") # Read neg-log EDC value B06-665C4 from T1 complex sequence
length=217892
```

Score = 39.2 bits (15%), Expect = 39
 Identical = 15/15 (100%), Gaps = 0/15 (0%)
 Standard-BLAST/PSM

| | | | |
|-------|------|-------------------|------|
| Query | 2 | TGTTCAAGCTTCAAGCA | 26 |
| | | | |
| SLYCL | 5730 | TGTTCAAGCTTCAAGCA | 5746 |

> [U000000000](#)  human DNA sequence from clone 82-696A7 on chromosome q21.1-41.2
containing the 3' end of the *IGFBP3* gene for integral membrane
protein 3A and a kinase family member 82-7276A1 protoyeptet.
complete sequence

Score = 30.2 bits (75), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Standard-Plus/XMing

| | | | |
|---------|-------|------------------|-------|
| Query | 1 | TGTCATACGCTGACCA | 16 |
| | | + | |
| Subject | 55852 | TGTCATACGCTGACCA | 55852 |


▶ [NM_003336.2](#) Human DNA sequence from clone HFL1-54706 on chromosome 1. Contains the 5' end of the gene for a novel protein (PRL1A15), a ribosomal protein L18 (PRL1) pseudogene, the DMT1 gene for divalent metal 1, the 5' end of a ribosomal protein L23a (PRL13a) pseudogene and a CpG island, complete sequence (length=14396)

Score = 99.2 bits (10), Expect = 39
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strandings: 2/15

```

Query :      TGTAAAGCTGACCA  16
          |||||
S104L 55046 TGTAAAGCTGACCA  55123

```

▣ [Download](#)  *Scaldfingis thelensis* chromosome 2 clone TIF04 exp. nt95, complete
sequence
Length=11401

Score = 39.2 bits (15%), Expect = 39
 Identity = 15/15 (100%), Gaps = 0/15 (0%)
 GetOrder2app/F/seq

| | | | |
|--------|-------|----------------|-------|
| Query | 7 | TGTCAGAGCCAGCA | 15 |
| | | | |
| RefSeq | TG033 | TGTCAGAGCCAGCA | 70635 |

20040717.11  *Amelobaptis thaisana* chromosome 2 clone (1324 x60298, *contig*)
3000000
1000000000

Score = 30.7 bits (15), Expect = 35
Identical = 17/37 (46%), Gaps = 0/35 (0%)
Strand: 5' to 3'

| | | |
|---------------|-----------------|------|
| Query 2 | TGTTAAAGCTAAGCA | 28 |
| | | |
| Subject 12919 | TGTTAAAGCTAAGCA | 7290 |

doi:10.1371/journal.pone.0140574.g005

2003.03.24

```
Score = 39.2 bits (11), Expect = 36
(coverage = 19/31 = 61%), Sequ = 0/15 (0%)
Nucleotide: 0/15 = 0.00%
```

| | | | |
|-----------|-------|----------------|-------|
| Genotype | 2 | TGTTAAGGCTAAGA | 36 |
| | | | |
| Reference | 29782 | TGTTAAGGCTAAGA | 25789 |

[illegible][illegible]

Score = 30.2 bits (11), Expect = 35
 (fontsize = 10/35, 1002), Seps = 0/15 (0)
 Standardize/Print

| | | | |
|-------|-----|---------------|-----|
| Genes | 1 | GTGCTGAGCCGAC | 75 |
| | | | |
| Genes | 326 | GTGTGAGCCGAC | 376 |

■ [raai190903.0.2100000002](#) *Leptocarpus nigroviridis* full-length cDNA
Length: 562

2007, 2008, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 2681, 2682, 2683, 2684, 2685, 2686, 2687, 2688, 2689, 26

Score = 30.2 bits (15), Expect = 36
(font) size = 19/15 = 100%, Segs = 0/15 (0%)
Standard-Plus/Plus

| | | | |
|--------|-----|-----------------|-----|
| Query | 1 | GTGTCAGAGCTGAGC | 75 |
| | | | |
| RefSeq | 574 | GTGTCAGAGCTGAGC | 574 |

■ *Stilpnocladia* ■ *Oryza sativa* (japonica cultivar-group) genomic DNA, chromosome

UDC 62-50:72.6.94.73.2

score alignment for this subject sequence by:
2 votes above threshold location
score start location, subject score location

Features relating this part of subject sequence:
 1000 00 00 0 0 000 0000000000
 0000 00 00 0 0 000 0000000000

Score = 30.2 bits (15%, Expect = 35
(identities = 19/25 = 76%), Segs = 0/15 (0%
Stamps = 0/15 = 0%)

```

Query: 2      TTTTAAAGCCAAAC  16
          |||||
Subject: 176752 TTTTAAAGCCAAAC  7552504

```

Features in this part of subject sequence:

Score = 29.1 bits (14, Expect = 15)
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Sequences = 2

| | | | |
|---------|----------|-----------------|----------|
| Query | 5 | GCCTGAGGCTCAACA | 16 |
| | | | |
| Subject | 24424694 | GCCTAGGCTCAACA | 24454757 |

D *Debaromyces hawaiiensis* microorganism F of strain C8597 of Eubazymycetes

Page 401
Langens 229604

Sort alignments for this project sequence by:
 R value
 Asc, Desc, Similar, Dissim, Start position

Features in this part of subject sequence:
100-1000, 1000-1000, 1000-1000

```

@font-face {
  font-family: 'Baskerville';
  src: url('Baskerville.woff2') format('woff2'),
       url('Baskerville.woff') format('woff'),
       url('Baskerville.ttf') format('truetype');
}

```

| | | |
|--------------|----------------|--------|
| Q92V_2 | TATCAGAGCCAGAC | 16 |
| | | |
| Abiet_51952w | TATCAGAGCCAGAC | 51952z |

Features in this part of subject sequence:
 ANONYMOUS, JOURNAL, DURING

```
Source = 05.5' data (13%, Exp = 632)
Identities = 13/13 (100%), Cons = 0/13 (0%)
Residue05.5' data
```

| | | |
|---------------|------------------|--------|
| Query 6 | VERBODEN TOEGANG | To |
| | VERBODEN TOEGANG | |
| Object 712549 | VERBODEN TOEGANG | 712549 |

> **chrUCR23:kb1**: chrucpizellula baltica OM 1 complete genome; segment 2/4
Length=76449

2007/08/26 10:00

Features in *ham part of subject sequence:
 :mathematical :mathematical :mathematical :mathematical

Contig = 30.2 bits (15), Expect = 38
Identifiers = 15/15 (100%), Gaps = 0/15 (0%)
Strand=plus/minus

```
Query 7: TTTTAAATCTGAGACG 16  
        TTTTTTTTTTTTTTTT  
Objet: 157737 TGTCCAGGCCTAACG 157740
```

g1221222.11 This sequence chromosome 3, clone BP24-357A22, complete sequence

Language = 152762

Count = 30.7 bits (15, Export = 33
Identical = 15/15 (100%), Gen = 0/15 (0%)
Strands=0/00/0/00

COPY 2 T67028ABTCA-2C4 25
1111111111

